

GenCore version 5.1.6  
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# OM nucleic - nucleic search, using sw model

Run on: January 15, 2004, 11:20:12 ; Search time 279.4 Seconds

(without alignments)  
2635.552 Million cell updates/sec

Title: US-10-062-875a-5

Perfect score: 18

Sequence: 1 ggcatatcaacgggtga 18

Scoring table: IDENTITY\_NTC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 segs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmb1.\*

1: gb\_ba.\*

2: gb\_hcg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_hcg\_hum.\*

31: em\_hcg\_inv.\*

32: em\_hcg\_other.\*

33: em\_hcg\_mus.\*

34: em\_hcg\_pln.\*

35: em\_hcg\_rtd.\*

36: em\_hcg\_mam.\*

37: em\_hcg\_vrt.\*

38: em\_sy.\*

39: em\_hugo\_hum.\*

40: em\_hugo\_mus.\*

41: em\_hugo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	1306	1	BPI51001
2	16.4	91.1	12598	1	AE0147223
3	16.4	91.1	129302	8	AC133778
4	16.4	91.1	136321	8	AP003300
5	16.4	91.1	138701	8	AP003243
6	16.4	91.1	163795	8	CNS05TEU
7	16.4	91.1	164236	8	AC133339
8	16.4	91.1	168896	2	OSTN00285
9	16.4	91.1	300115	1	AP005076
10	16.4	91.1	349980	6	AX492784
11	16.4	91.1	349980	6	AX492785
12	16.4	91.1	349980	6	AX553951
13	16.4	91.1	349980	6	AX553952
14	15.4	85.6	2814	3	AX351522
15	15.4	85.6	2814	3	AX351522
16	15.4	85.6	55163	3	AC006605
17	15.4	85.6	76396	2	AC012995
18	15.4	85.6	90689	2	AC141010
19	15.4	85.6	94225	2	AC138542
20	15.4	85.6	153205	2	AP004552
21	15.4	85.6	154881	2	AP005919
22	15.4	85.6	190801	2	AC009212
23	15.4	85.6	294850	1	AE627268
24	15.4	85.6	301983	1	AE016840
25	15.4	85.6	303432	3	AE003604
26	15.4	85.6	322194	8	CNS0594S
27	15	83.3	1474	6	165498
28	15	83.3	1474	6	190341
29	15	83.3	1474	8	CHU39834
30	15	83.3	2053	14	AP235166
31	15	83.3	2056	1	AE008885
32	15	83.3	96086	1	STY5TMD1
33	15	83.3	125646	2	AC137986
34	15	83.3	169547	10	AL590503
35	15	83.3	258050	1	AL627278
36	15	83.3	299991	1	AE016845
37	14.8	82.2	400	11	G16871
38	14.8	82.2	690	6	AX392266
39	14.8	82.2	952	8	AY261522
40	14.8	82.2	1233	1	AF273254
41	14.8	82.2	1481	4	AY240020
42	14.8	82.2	1659	6	AX189037
43	14.8	82.2	1867	1	EC5RMB
44	14.8	82.2	2000	6	AX508239
45	14.8	82.2	2186	8	AF024625

## ALIGNMENTS

RESULT 1

LOCUS BPI51001

DEFINITION B.parapertusis insertion sequence IS1001 tnpa gene for transposase.

ACCESSION X66858.1

VERSION X66858.1

KEYWORDS insertion sequence; insertion sequence IS1001; tnpa gene; transposase.

SOURCE Bordetella parapertusis

ORGANISM Bordetella parapertusis

REFERENCE 1 van der Zee, A., Agterberg, C., van Agterveld, M., Peeters, M. and

TITLE  
Mool, F.R.  
Characterization of IS1001, an insertion sequence element of  
Bordetella parapertussis  
J. Bacteriol. 175 (1), 141-147 (1993)

JOURNAL  
MEDLINE  
93106948  
PUBMED  
8093238  
REFERENCE  
2 (bases 1 to 1306)  
AUTHORS  
Van der Zee, A.  
TITLE  
Direct Submision  
Submitted (12-JUN-1992) A. Van Der Zee, National Institute of Health  
JOURNAL  
Environmental Protection, A Van Leeuwenhoeklaan 9, P O Box 1,  
3720 BA Bilthoven, THE NETHERLANDS  
COMMENT  
On Jul 10, 2002 this sequence version replaced gi:262329.  
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Best Local Similarity 100.0%; Pred. No. 14;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGCATATCAACGGGTGA 18  
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Db 375 GCGCATATCAACGGGTGA 392

RESULT 2  
AE014723 12598 bp DNA linear BCT 31-OCT-2002  
LOCUS  
AE014723.c  
DEFINITION  
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genome.  
ACCESSION  
AE014723 AE014295  
VERSION  
AE014723.1 GI:23326232  
KEYWORDS  
Bifidobacterium longum NCC2705  
Bifidobacterium longum NCC2705  
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;  
Bifidobacteriaceae; Bifidobacterium.  
SOURCE  
Schell, M.A., Kamilrantzou, M., Snel, B., Vilanova, D., Berger, B.,  
Pessi, G., Zwielen, M.-C., Desiere, F., Bork, P., Delley, M.,  
Pridmore, D. and Arigoni, F.  
ORGANISM  
The genome sequence of Bifidobacterium longum reflects its  
adaptation to the human gastrointestinal tract  
Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14422-14427 (2002)  
PUBMED  
12381787  
JOURNAL  
2 (bases 1 to 12598)  
AUTHORS  
Schell, M.A., Kamilrantzou, M., Snel, B., Vilanova, D., Berger, B.,

TITLE  
Pessi, G., Zwielen, M.-C., Desiere, F., Bork, P., Delley, M.,  
Pridmore, D. and Arigoni, F.  
Direct Submision  
Submitted (27-AUG-2002) Bioscience, Nestle Research Center, P.O.  
Box 44, Lausanne 26 1000, Switzerland  
JOURNAL  
MEDLINE  
93106948  
PUBMED  
8093238  
REFERENCE  
2 (bases 1 to 12598)  
AUTHORS  
Van der Zee, A.  
TITLE  
Direct Submision  
Submitted (12-JUN-1992) A. Van Der Zee, National Institute of Health  
JOURNAL  
Environmental Protection, A Van Leeuwenhoeklaan 9, P O Box 1,  
3720 BA Bilthoven, THE NETHERLANDS  
COMMENT  
On Jul 10, 2002 this sequence version replaced gi:262329.  
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/note="COG family: sensory transduction histidine kinases;

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: January 15, 2004, 11:20:12 ; Search time 294.922 Seconds  
(without alignments)  
2635.552 Million cell updates/sec

Title: US-10-062-875A-6

Perfect score: 19  
Sequence: 1 caggsgcaactgcgtccatc 19

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 20454813366 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenBank:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pac:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vi:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rtd:\*

36: em\_htg\_mam:\*

37: em\_htg\_vit:\*

38: em\_sy:\*

39: em\_htgo\_hum:\*

40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	1306	1	BPI1001
2	17.4	91.6	7021	1	AF019635
3	17.4	91.6	7109	1	PF041301
4	17.4	91.6	1461	1	AF043544
5	17.4	91.6	1806	9	AC079403
6	17	89.5	16644	1	AE006918
7	17	89.5	20760	1	MGCV21D4
8	17	89.5	38721	1	MGCV219
9	17	89.5	138829	2	HSC0001236
10	17	89.5	343050	1	BX248334
11	16.4	86.3	588	11	G79512
12	16.4	86.3	2596	4	AF111535
13	16.4	86.3	10333	1	AE006873
14	16.4	86.3	12421	1	AE000943
15	16.4	86.3	70360	2	AC101122
16	16.4	86.3	70571	2	AC145071
17	16.4	86.3	99761	8	AC006161
18	16.4	86.3	101284	8	ATAC009991
19	16.4	86.3	103517	8	AC073395
20	16.4	86.3	105795	1	SYCCPNC
21	16.4	86.3	120648	8	AP003859
22	16.4	86.3	169284	5	AL953899
23	16.4	86.3	216491	2	AC128110
24	16.4	86.3	231157	2	AC111347
25	16.4	86.3	254989	2	AC107773
26	16.4	86.3	259783	2	AC111985
27	16	84.2	321	6	BD077656
28	16	84.2	640	6	BD082462
29	16	84.2	855	6	E14996
30	16	84.2	1341	9	BC012415
31	16	84.2	1358	9	HS12478
32	16	84.2	1374	6	BD082403
33	16	84.2	1529	6	BD082463
34	16	84.2	2491	10	BC031769
35	16	84.2	4943	6	E14999
36	16	84.2	8481	1	AB010691
37	16	84.2	74355	1	AY120853
38	16	84.2	135578	9	AF064861
39	16	84.2	153679	2	EX000987
40	16	84.2	154523	2	EX005217
41	16	84.2	301442	1	AB016798
42	16	84.2	340000	9	HS21C079
43	15.8	83.2	309	1	RHNMOMMA
44	15.8	83.2	481	11	G97381
45	15.8	83.2	658	11	BV076785

## ALIGNMENTS

RESULT 1  
BPI1001/c  
LOCUS 1306 bp DNA linear BCT 07-JUL-2002  
DEFINITION B:parapertussis insertion sequence IS1001 tnpa gene for  
transposase.  
ACCESSION X66858.1  
VERSION X66858.1 GI:39755  
KEYWORDS insertion sequence; insertion sequence IS1001; tnpa gene;  
transposase.  
SOURCE Bordetella parapertussis  
ORGANISM Bordetella parapertussis  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella.  
REFERENCE 1  
AUTHORS van der Zee A., Agterberg C., van Agterveld M., Peeters M. and

TITLE Mool, F.R.  
 Characterization of IS1001, an insertion sequence element of  
 Bordetella parapertussis  
 J. Bacteriol. 175 (1), 141-147 (1993)  
 JOURNAL MEDLINE  
 93106948  
 PUBLISHED 80932238  
 REFERENCE 2 (bases 1 to 1306)  
 AUTHORS van der Zee, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-JUN-1992) A. Van Der Zee, National Institute of Health  
 & Environmental Protection, A Van Leeuwenhoeklaan 9, P O Box 1,  
 3720 BA Bilthoven, THE NETHERLANDS  
 COMMENT On Jul 10, 2002 this sequence version replaced gi:262329.  
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 Best Local Similarity 100.0%; Pred No. 17;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CAGGGCAAACTCGTCATC 19  
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 Db 574 CAGGGCAAACTCGTCATC 556  
 RESULT 2  
 AF019635/c 7021 bp DNA linear BCT 21-SEP-1997  
 LOCUS  
 DEFINITION  
 AF019635 Pseudomonas putida TOL plasmid pDK1 xyIU, benzyl alcohol  
 dehydrogenase (xyIU), benzaldehyde dehydrogenase (xyIC), xyIene  
 monooxygenase hydroxylase component (xyIM), and xyIene  
 monooxygenase electron transfer component (xyIA) genes, complete  
 cds.  
 AF019635  
 VERSION AF019635.1 GI:2425076  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Pseudomonas putida  
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 Pseudomonadaceae; Pseudomonas.  
 REFERENCE  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2004, 11:20:12 : Search time 372.533 Seconds

(without alignments) 2635.552 Million cell updates/sec

Title: US-10-062-875A-7

Perfect score: 24

Sequence: 1 gttcttcgaactgggtgcatcac 24

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

GenBank:\*

1: gb\_ba:\*

2: gb\_hlg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

15: em\_da:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_ov:\*

22: em\_ov:\*

23: em\_ph:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vi:\*

30: em\_hlg\_hum:\*

31: em\_hlg\_inv:\*

32: em\_hlg\_other:\*

33: em\_hlg\_mus:\*

34: em\_hlg\_pln:\*

35: em\_hlg\_rtd:\*

36: em\_hlg\_man:\*

37: em\_hlg\_vtl:\*

38: em\_sy:\*

39: em\_hgo\_hum:\*

40: em\_hgo\_mus:\*

41: em\_hgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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2	20.8	86.7	73800	1 AF286216
3	19.8	82.5	5307	6 AX276469
4	19.8	82.5	311143	1 AB016762
5	18.4	76.7	17277	1 AF237701
6	18.4	76.7	161005	2 AC116595
7	18.4	76.7	172114	10 AC121903
8	18.2	75.8	1042	1 AY228241
9	18.2	75.8	1305	1 AF285835
10	18.2	75.8	4620	6 AX078429
11	18.2	75.8	34244	1 AOBPCZA363
12	18.2	75.8	40430	1 AB107223
13	18.2	75.8	85237	9 HSDJ653C5
14	18.2	75.8	93829	3 AC007122
15	18.2	75.8	119163	9 AC119675
16	18.2	75.8	121414	2 AC017234
17	18.2	75.8	173165	3 AC099005
18	18.2	75.8	174673	9 AC019187
19	18.2	75.8	174822	9 AC013275
20	18.2	75.8	182560	3 AC099024
21	18.2	75.8	189023	9 AL592114
22	18.2	75.8	191240	2 AC027738
23	18.2	75.8	204207	2 AC023147
24	18.2	75.8	217586	2 AC016076
25	18.2	75.8	262533	3 AE003809
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32	17.8	74.2	150114	2 AC074004
33	17.8	74.2	156313	2 AC141774
34	17.8	74.2	169892	9 AC068397
35	17.8	74.2	184489	2 AC027771
36	17.8	74.2	189622	9 AC116442
37	17.8	74.2	211441	2 AC130659
38	17.8	74.2	214166	9 AC009660
39	17.8	74.2	215084	2 BX248502
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42	17.8	74.2	272761	2 AC094657
43	17.8	74.2	313450	1 AU596170
44	17.8	74.2	319630	6 AX413016
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## ALIGNMENTS

RESULT 1

LOCUS BPIS1001

DEFINITION B.parapertussis insertion sequence IS1001 tnpA gene for transposase.

ACCESSION X66858.1 GI:39755

VERSION X66858.1

KEYWORDS insertion sequence; insertion sequence IS1001; tnpA gene; transposase.

SOURCE Bordetella parapertussis

ORGANISM Bordetella parapertussis

REFERENCE 1 van der Zee, A., Agterberg, C., van Agterveld, M., Peeters, M. and

TITLE Mooi, F.R.  
Characterization of IS1001, an insertion sequence element of  
Bordetella parapertussis  
JOURNAL J. Bacteriol. 175 (1), 141-147 (1993)  
MEDLINE 93106948  
PUBMED 8093238  
REFERENCE 2 (bases 1 to 1306)  
AUTHORS van der Zee, A.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-1992) A. Van Der Zee, National Institute of Health  
& Environmental Protection, A Van Leeuwenhoeklaan 9, P O Box 1,  
3720 BA Bilthoven, THE NETHERLANDS  
COMMENT On Jul 10, 2002 this sequence version replaced gi:262329.  
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DB 457 GTTCTCGAACTGGGTTGGCATAC 480  
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LOCUS Pseudomonas syringae pv. syringae syringopeptin synthetase (sypp),  
DEFINITION syringopeptin synthetase B (sypp), and syringopeptin synthetase C  
(syppC) genes, complete cds.  
ACCESSION AF286216  
VERSION AF286216.2 GI:29165621  
KEYWORDS Pseudomonas syringae pv. syringae  
SOURCE Pseudomonas syringae pv. syringae  
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Pseudomonadaceae; Pseudomonas.  
REFERENCE 1 (bases 1 to 3920)  
AUTHORS Scholz-Schroeder, B.K., Hutchison, M.L., Grgurina, I. and Gross, D.C.  
TITLE The contribution of syringopeptin and syringomycin to virulence of  
Pseudomonas syringae pv. syringae strain B301D on the basis of sypp  
and sypp1 biosynthesis mutant analysis  
JOURNAL Mol. Plant Microbe Interact. 14 (3), 336-348 (2001)  
MEDLINE 21171030  
PUBMED 11377431  
REFERENCE 2 (bases 1 to 73800)

AUTHORS Scholz-Schroeder, B.K., Soule, J.D. and Gross, D.C.  
TITLE The sypp, syppB, and syppC synthetase genes encode twenty-two modules  
involved in the nonribosomal peptide synthesis of syringopeptin by  
Pseudomonas syringae pv. syringae B301D  
JOURNAL Mol. Plant Microbe Interact. 16, 271-280 (2003)  
REFERENCE 3 (bases 1 to 3920)  
AUTHORS Scholz-Schroeder, B.K., Soule, J.D., Grgurina, I. and Gross, D.C.  
TITLE Direct Submission  
JOURNAL Submitted (11-JUL-2000) Department of Plant Pathology, Washington  
State University, P.O. Box 646430, Pullman, WA 99163-6430, USA  
4 (bases 1 to 73800)  
AUTHORS Scholz-Schroeder, B.K., Soule, J.D. and Gross, D.C.  
TITLE Direct Submission  
JOURNAL Submitted (26-NOV-2002) Department of Plant Pathology, Washington  
State University, P.O. Box 646430, Pullman, WA 99163-6430, USA  
COMMENT Sequence update by submitter  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: January 15, 2004, 11:20:12 ; Search time 341.489 Seconds

(without alignments)  
2635.552 Million cell updates/sec

Title: US-10-062-875A-8

Sequence: 1 gtcaagacgtcgagcaagctc 22

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

GenBank1:  
1: gb\_ba:\*  
2: gb\_hg:\*  
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41: gb\_ov:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
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3	18.8	85.5	302050	1 AP093526
4	18.4	83.6	299910	1 AP005957
5	17.8	80.9	522	5 AF125049
6	17.8	80.9	522	5 AF125049
7	17.8	80.9	12946	1 AE013592
8	17.8	80.9	95660	2 AC131181
9	17.8	80.9	98914	2 AC114724_3
10	17.8	80.9	110000	2 AC114724_2
11	17.8	80.9	142372	9 AC132152
12	17.8	80.9	151829	2 AC132880
13	17.8	80.9	156817	9 AC009406
14	17.8	80.9	158341	9 AC021733
15	17.8	80.9	158430	2 AC012431
16	17.8	80.9	162577	2 AL954709
17	17.8	80.9	186233	9 AC092329
18	17.8	80.9	189317	2 AC024483
19	17.8	80.9	199208	2 AC134427
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22	17.4	79.1	1625	6 AX399907
23	17.4	79.1	1653	9 HSA430K20
24	17.4	79.1	1671	9 AF449218
25	17.4	79.1	11589	1 AB009650
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27	17.4	79.1	79516	9 AC004834
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30	17.4	79.1	199658	2 AC133053
31	17.4	79.1	210359	9 HSA430K20
32	17.4	79.1	223442	10 AL662804
33	17.4	79.1	239464	2 AC103079
34	17.4	79.1	242506	2 AC094821
35	17.2	78.2	2736	10 BC014812
36	17.2	78.2	12531	1 AB011897
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38	17.2	78.2	2781	1 AF030414
39	17.2	78.2	64924	1 AC118046
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43	17.2	78.2	105872	2 LMFC1993
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45	17.2	78.2	126394	9 AC109998

## ALIGNMENTS

Result No.	Score	* Query Match Length	DB ID	Description
1	22	100.0	1306	1 BPIS1001
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3	18.8	85.5	302050	1 AP093526
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7	17.8	80.9	12946	1 AE013592
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9	17.8	80.9	98914	2 AC114724_3
10	17.8	80.9	110000	2 AC114724_2
11	17.8	80.9	142372	9 AC132152
12	17.8	80.9	151829	2 AC132880
13	17.8	80.9	156817	9 AC009406
14	17.8	80.9	158341	9 AC021733
15	17.8	80.9	158430	2 AC012431
16	17.8	80.9	162577	2 AL954709
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19	17.8	80.9	199208	2 AC134427
20	17.8	80.9	252115	2 AC031854
21	17.8	80.9	254538	2 AC097032
22	17.4	79.1	1625	6 AX399907
23	17.4	79.1	1653	9 HSA430K20
24	17.4	79.1	1671	9 AF449218
25	17.4	79.1	11589	1 AB009650
26	17.4	79.1	13813	1 AB014610
27	17.4	79.1	79516	9 AC004834
28	17.4	79.1	118106	2 AC110867
29	17.4	79.1	170382	2 AC101772
30	17.4	79.1	199658	2 AC133053
31	17.4	79.1	210359	9 HSA430K20
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33	17.4	79.1	239464	2 AC103079
34	17.4	79.1	242506	2 AC094821
35	17.2	78.2	2736	10 BC014812
36	17.2	78.2	12531	1 AB011897
37	17.2	78.2	13829	1 AB005935
38	17.2	78.2	2781	1 AF030414
39	17.2	78.2	64924	1 AC118046
40	17.2	78.2	79676	8 AC090435
41	17.2	78.2	98221	9 AL161940
42	17.2	78.2	102653	8 AC090436
43	17.2	78.2	105872	2 LMFC1993
44	17.2	78.2	110000	2 LMFC1993
45	17.2	78.2	126394	9 AC109998

REFERENCE  
AUTHORS  
van der Zee, A., Agterberg, C., van Agterveld, M., Peeters, M. and

Moel, F.R.  
Characterization of IS1001, an insertion sequence element of  
Bordetella parapertussis  
J. Bacteriol. 175 (1), 141-147 (1993)

JOURNAL  
MEDLINE  
93106948  
PUBMED  
8093238  
2 (bases 1 to 1306)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (12-JUN-1992) A. Van Der Zee, National Institute of Health  
& Environmental Protection, A Van Leeuwenhoeklaan 9, P O Box 1,  
3720 BA Bilthoven, THE NETHERLANDS  
On Jul 10, 2002 this sequence version replaced gi:262329.

COMMENT  
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BASE COUNT 269 a 371 c 420 g 246 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 GTCAAGACGCTGGACACAGCTC 22  
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LOCUS Bos taurus clone RP42-331024, WORKING DRAFT SEQUENCE, 6 ordered  
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AC130788.2 GI:22748398  
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Bos taurus  
Bos taurus  
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Bovidae; Bovinae; Bos.  
1 (bases 1 to 216844)  
Akhter N., Antonellis A., Ayele K., Beckstrom-Sternberg S.M.,  
Benjamin B., Blakesley R.W., Bouffard G.G., Breen K., Brinkley C.,  
Brooks S., Dietrich N.L., Granite S., Guan X., Gupta J.,  
Haghighi P., Han J., Hansen N., Ho S.-L., Idol J.R., Karlins E.,  
Latic P., Lee-Lin S.-O., Legaapi R., Maduro O.L., Maduro V.B.,  
Marques E.H., Masello C., Maskeri B., Masrrian S.D.,  
McCluskey J.C., McDowell J., Pagitirigan C., Pearson R.,  
Portnoy M.E., Prasad A., Reddix-Dugue N., Schneider M.G., Sison C.,

Stantipop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,  
Wehrby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
2 (bases 1 to 216844)  
Green, E.D.  
Direct Submission  
Submitted (14-AUG-2002) NIH Intramural Sequencing Center, 8717  
Groveomont Circle, Gathersburg, MD 20877, USA  
3 (bases 1 to 216844)  
Green, E.D.  
Direct Submission  
Submitted (06-SEP-2002) NIH Intramural Sequencing Center, 8717  
Groveomont Circle, Gathersburg, MD 20877, USA  
On Sep 6, 2002 this sequence version replaced gi:22218458.

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Location/Qualifiers  
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The sequence data in this record represents an 'enhanced'  
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order and orientation of each sequence contig has been  
established using one or more of the following: read-pair  
data from individual subclones, overlaps with neighboring  
clones, alignment with available reference sequence (e.g.,  
human), and/or confirmation by PCR testing. In addition,  
the sequence assembly is based on at least 8x average  
coverage in Q20 bases and has been reviewed to rule out  
gross misassemblies, the low-quality ends of sequence  
contigs have been trimmed away, and each base is associated  
with a Phrap-derived quality score.

----- Summary Statistics -----  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 215115 bases at least Q40  
Consensus quality: 215785 bases at least Q20  
Insert size: 208000; agarose-fp  
Insert size: 216344; sum-of-contigs  
Quality coverage: 8.45x in Q20 bases; agarose-fp  
Quality coverage: 8.12x in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* been provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

1 53614: contig of 53614 bp in length  
53615 53714: gap of unknown length  
53715 132668: contig of 78954 bp in length  
132669 132768: gap of unknown length  
132769 150539: contig of 17771 bp in length  
150540 150639: gap of unknown length  
150640 184327: contig of 33687 bp in length  
184327 184426: gap of unknown length  
184427 187144: contig of 2718 bp in length  
187145 187244: gap of unknown length  
187245 216844: contig of 29600 bp in length.



BOLLEN ALEX (BE) ; GODEROID EDMOND (BE) ; UNIV BRUXELLES (BE) ;  
FAUCONNIER ALAIN (BE)

## FEATURES

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BASE COUNT 174 a 350 c 269 g 158 t  
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Query Match 100.0%; Score 18; DB 6; Length 951;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGTTCCTCAAGAGCG 18  
Db 582 CCAGTTCCTCAAGAGCG 599

RESULT 2  
LOCUS AF349431 1010 bp DNA linear BCT 11-MAY-2001  
DEFINITION Bordetella holmesii IS481-like insertion sequence, partial  
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ACCESSION AF349431  
VERSION AF349431.1 GI:13384215  
SOURCE  
ORGANISM  
Bordetella holmesii  
Bordetella holmesii  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella.  
1 (bases 1 to 1010)  
Reischl, U., Lehn, N., Sanden, G.N. and Loeffelholz, M.J.  
Real-time PCR assay targeting IS481 of Bordetella pertussis and  
molecular basis for detecting Bordetella holmesii  
J. Clin. Microbiol. 39 (5), 1963-1966 (2001)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
11326023  
2 (bases 1 to 1010)  
Reischl, U., Loeffelholz, M.J. and Sanden, G.N.  
Direct Submission  
Submitted (14-FEB-2001) Institute of Medical Microbiology and  
Hygiene, University of Regensburg, Franz-Josef-Strauss-Allee 11,  
Regensburg D-93053, Germany  
LOCATION/Qualifiers  
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/mol\_type="genomic DNA"  
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/db\_xref="taxon:35814"  
/insertion\_seq="IS481-like"  
BASE COUNT 185 a 365 c 288 g 170 t 2 others

Db 673 CCAGTTCCTCAAGAGCG 690

## FEATURES

Location/Qualifiers  
1053 bp DNA linear BCT 26-APR-1993  
B.pertussis insertion sequence with 28 bp terminal inverted repeats  
DNA.

ACCESSION M22031.1 GI:144060  
VERSION M22031.1  
KEYWORDS  
SOURCE  
ORGANISM  
Bordetella pertussis  
Bordetella pertussis  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella.  
1 (bases 1 to 1053)  
McLafferty, M.A., Hargus, D.R. and Hewlett, E.L.  
Nucleotide sequence and characterization of a repetitive DNA  
element from the genome of Bordetella pertussis with  
characteristics of an insertion sequence  
J. Gen. Microbiol. 134 (Pt 8), 2297-2306 (1988)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
2908119  
Original source text: B.pertussis DNA.  
Location/Qualifiers  
1..1053  
/organism="Bordetella pertussis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:520"

repeat\_region 1..28  
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BASE COUNT 201 a 375 c 296 g 181 t  
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Query Match 100.0%; Score 18; DB 1; Length 1053;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGTTCCTCAAGAGCG 18  
Db 684 CCAGTTCCTCAAGAGCG 701

RESULT 4  
LOCUS S66929 1053 bp DNA linear BCT 13-JAN-1994  
DEFINITION {inverted repeating element RSBP1} [Bordetella pertussis, Genomic,  
1053 nt].  
ACCESSION S66929  
VERSION S66929.1 GI:440882  
KEYWORDS  
SOURCE  
ORGANISM  
Bordetella pertussis  
Bordetella pertussis  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella.  
1 (bases 1 to 1053)  
Kiriilov, M.I., Shumkov, Iu.L., Nechaeva, E.V., Sinashina, L.N. and  
Karataev, G.I.  
Nucleotide sequence and properties of an inverted repeating element  
of a Bordetella pertussis chromosome  
Genetika 29 (8), 1267-1277 (1993)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
8405971  
GenBank staff at the National Library of Medicine created this  
entry [NCBI gi35813922]. From the original journal article.  
This sequence comes from Fig. 4.  
Location/Qualifiers  
1..1053  
/organism="Bordetella pertussis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:520"

## FEATURES

source  
Query Match 100.0%; Score 18; DB 1; Length 1010;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAGTTCCTCAAGAGCG 18  
|||||

SEQ ID NO:1

SEQ ID NO. 2

BOULEN ALEX (BE) ; GODFROID EDMOND (BE) ; UNIV BRUXELLES (BE) ;  
FAUCONNIER ALAIN (BE)  
FEATURES  
Source  
Location/Qualifiers  
1..951  
/organism="Bordetella pertussis"  
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/db\_xref="taxon:520"

## CDS

1..951  
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WLPFLAQGQGLADASSRPTVSPRIAPAKLAIVELRKRLTQARIADLVASST  
VSRVLAAGISHLADPAEPVRYEHOAPGLHIDIKKGRIGRPHRTGNRDT  
VEGAWDFVAFIDHARVAFDHPDERFPAVDFLDVAYVYRLGVTLLTN  
GSAFRSPAALCHELGIGIKRFTPYRPTQNKRFIQSALREWAVAHYVQNSQHRA  
DAMKSMTHNMHMRPHOGIGRAVPIGRILNLDENVLLTVHT"

BASE COUNT 174 a 350 c 269 g 158 t

ORIGIN

Query Match 100.0%; Score 23; DB 6; Length 951;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 GAGTTCTGTAGGTGAGCGTA 23  
DB 815 GAGTTCTGTAGGTGAGCGTA 793

RESULT 2  
AF349431/c 1010 bp DNA linear BCT 11-JAN-2001  
LOCUS  
DEFINITION Bordetella holmesii IS481-like insertion sequence, partial  
sequence.  
ACCESSION AF349431  
VERSION AF349431.1 GI:13384215  
KEYWORDS  
SOURCE Bordetella holmesii  
ORGANISM Bordetella holmesii  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella.

REFERENCE  
AUTHORS Reischl, U., Lehn, N., Sanden, G.N. and Loeffelholz, M.J.  
TITLE Real-time PCR assay targeting IS481 of Bordetella pertussis and  
molecular basis for detecting Bordetella holmesii

JOURNAL J. Clin. Microbiol. 39 (5), 1963-1966 (2001)  
MEDLINE 21225601  
PUBMED 11326023  
2 (bases 1 to 1010)  
Reischl, U., Loeffelholz, M.J. and Sanden, G.N.  
Direct Submission  
Submitted (14-FEB-2001) Institute of Medical Microbiology and  
Hygiene, University of Regensburg, Franz-Josef-Strauss-Allee 11,  
Regensburg D-93053 Germany  
Location/Qualifiers  
1..1010  
/organism="Bordetella holmesii"  
/mol\_type="genomic DNA"  
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/db\_xref="taxon:35814"  
/insertion\_seq="IS481-like"

BASE COUNT 185 a 365 c 288 g 170 t 2 others

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 1010;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 GAGTTCTGTAGGTGAGCGTA 23  
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DB 906 GAGTTCTGTAGGTGAGCGTA 884

RESULT 3  
BPTERRA/c  
LOCUS  
DEFINITION B.pertussis insertion sequence with 28 bp terminal inverted repeats  
DNA.  
ACCESSION M22031  
VERSION M22031.1 GI:144060  
KEYWORDS insertion sequence.  
SOURCE Bordetella pertussis  
ORGANISM Bordetella pertussis  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella.

REFERENCE  
AUTHORS McLafferty, M.A., Harcus, D.R. and Hewlett, E.L.  
TITLE Nucleotide sequence and characterization of a repetitive DNA  
element from the genome of Bordetella pertussis with  
characteristics of an insertion sequence

JOURNAL J. Gen. Microbiol. 134 (Pt 8), 2297-2306 (1988)  
MEDLINE 89310403  
PUBMED 2908119  
COMMENT Original source text: B.pertussis DNA.  
FEATURES  
Source  
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Location/Qualifiers  
/organism="Bordetella pertussis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:520"

repeat\_region 1..28  
/note="inverted repeat"  
repeat\_region 1026..1053  
/note="inverted repeat"

BASE COUNT 201 a 375 c 296 g 181 t

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 1053;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 GAGTTCTGTAGGTGAGCGTA 23  
DB 917 GAGTTCTGTAGGTGAGCGTA 895

RESULT 4  
S66929/c 1053 bp DNA linear BCT 13-JAN-1994  
LOCUS  
DEFINITION (inverted repeating element RSBp1) [Bordetella pertussis, Genomic,  
1053 nt].  
ACCESSION S66929  
VERSION S66929.1 GI:440882  
KEYWORDS  
SOURCE Bordetella pertussis  
ORGANISM Bordetella pertussis  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella.

REFERENCE  
AUTHORS Kirillov, M.Iu., Shumakov, Iu.L., Nechaeva, E.V., Siniashina, I.N. and  
Karataev, G.I.  
TITLE Nucleotide sequence and properties of an inverted repeating element  
of a Bordetella pertussis chromosome  
JOURNAL Genetika 29 (8), 1267-1277 (1993)  
MEDLINE 94010257  
PUBMED 8405971

REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gi2693 139922] from the original journal article.  
This sequence comes from Fig. 4.

FEATURES  
Source  
1..1053  
Location/Qualifiers  
/organism="Bordetella pertussis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:520"

CEQ 1020.3

FEATURES  
source  
BOLLEN ALEX (BE) ; GODFREID EDMOND (BE) ; UNIV BRUXELLES (BE) ;  
FAUCONNIER ALAIN (BE)

1..951  
Location/Qualifiers  
/organism="Bordetella pertussis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:520"

CDS  
1..951  
/note="unamed protein product"

BASE COUNT  
ORIGIN  
174 a 350 c 269 g 158 t

Query Match  
Best Local Similarity 100.0%; Score 28; DB 6; Length 951;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  
1 CACCGCTTACCGGACCTTACCGCCAC 28  
Db 712 CACCGCTTACCGGACCTTACCGCCAC 739

RESULT 2  
AF349431  
LOCUS  
DEFINITION  
Bordetella holmesii IS481-like insertion sequence, partial

ACCESSION  
AF349431  
VERSION  
AF349431.1 GI:13384215  
KEYWORDS  
SOURCE  
Bordetella holmesii  
Bordetella holmesii  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella.

REFERENCE  
AUTHORS  
Reischl, U., Lehn, N., Sanden, G. N. and Loeffelholz, M. J.  
TITLE  
Real-time PCR assay targeting IS481 of Bordetella pertussis and  
molecular basis for detecting Bordetella holmesii

JOURNAL  
J. Clin. Microbiol. 39 (5), 1963-1966 (2001)  
PUBMED  
21226021  
11326023  
2 (bases 1 to 1010)  
2 (bases 1 to 1010)  
Reischl, U., Loeffelholz, M. J. and Sanden, G. N.  
Direct Submission  
Submitted (14-FEB-2001) Institute of Medical Microbiology and  
Hygiene, University of Regensburg, Franz-Josef-Strauss-Allee 11,  
Regensburg D-93053, Germany

FEATURES  
source  
1..1010  
Location/Qualifiers  
/organism="Bordetella holmesii"  
/mol\_type="genomic DNA"

BASE COUNT  
ORIGIN  
185 a 365 c 288 g 170 t 2 others

Query Match  
Best Local Similarity 100.0%; Score 28; DB 1; Length 1010;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  
1 CACCGCTTACCGGACCTTACCGCCAC 28

Db 803 CACCGCTTACCGGACCTTACCGCCAC 830

RESULT 3

LOCUS  
DEFINITION  
B.pertussis insertion sequence with 28 bp terminal inverted repeats  
DNA.

ACCESSION  
M22031  
VERSION  
M22031.1 GI:144060  
KEYWORDS  
insertion sequence  
SOURCE  
Bordetella pertussis  
Bordetella pertussis  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella.

REFERENCE  
AUTHORS  
McLafferty, M. A., Harcus, D. R. and Hewlett, E. L.  
TITLE  
Nucleotide sequence and characterization of a repetitive DNA  
element from the genome of Bordetella pertussis with  
characteristics of an insertion sequence

JOURNAL  
J. Gen. Microbiol. 134 (Pt 8), 2297-2306 (1988)  
MEDLINE  
89310403  
PUBMED  
2908119

COMMENT  
Original  
source text: B.pertussis DNA.  
Location/Qualifiers

FEATURES  
source  
1..1053  
/organism="Bordetella pertussis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:520"

repeat\_region  
repeat\_region  
/note="inverted repeat"  
1026..1053  
/note="inverted repeat"

BASE COUNT  
ORIGIN  
201 a 375 c 296 g 181 t

Query Match  
Best Local Similarity 100.0%; Score 28; DB 1; Length 1053;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  
1 CACCGCTTACCGGACCTTACCGCCAC 28  
Db 814 CACCGCTTACCGGACCTTACCGCCAC 841

RESULT 4  
S66929  
LOCUS  
DEFINITION  
{inverted repeating element RSBp1} [Bordetella pertussis, Genomic,  
1053 nt].

ACCESSION  
S66929  
VERSION  
S66929.1 GI:440882  
KEYWORDS  
Bordetella pertussis  
Bordetella pertussis  
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
Alcaligenaceae; Bordetella.

REFERENCE  
AUTHORS  
Kirillov, M. Iu., Shumakov, Iu. L., Nechaeva, E. V., Sinfashina, L. N. and  
Karataev, G. I.  
TITLE  
Nucleotide sequence and properties of an inverted repeating element  
of a Bordetella pertussis chromosome

JOURNAL  
Genetika 29 (8), 1267-1277 (1993)  
MEDLINE  
94010257  
PUBMED  
8405971

REMARK  
Genbank staff at the National Library of Medicine created this  
entry [NCBI gi139922] from the original journal article.  
This sequence comes from Fig. 4.

FEATURES  
source  
1..1053  
Location/Qualifiers  
/organism="Bordetella pertussis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:520"

